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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2009; month=4; day=25; hr=13; min=28; sec=13; ms=988;]
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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2009; month=4; day=25; hr=13; min=26; sec=26; ms=876;]
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Application No: 10522388 Version No: 1.0

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<110> Ross, Richard
Sayers, Jon
Artymiuk, Peter

<120> Cytokine Polypeptides and Antiboidies Containing A Signal Sequence for the Attachment of Glycosylphosphatidyinositol

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<140> 10522388
<141> 2009-04-14

<150> 10/552,388
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<150> PCT/GB04/001572
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<150> GB 0324235.1
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<151> 2003-04-09

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<170> PatentIn version 3.5

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Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
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Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
130 135 140

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Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly
    210                 215                 220

Gly Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu
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<213> Artificial Sequence

<220>
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20 25 30

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Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
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Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
    50                  55                  60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65                  70                  75                  80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
                85                  90                  95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
            100                 105                 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
        115                 120                 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
    130                 135                 140

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Ser Gly Ser
225                 230                 235                 240

Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu Gln Ser
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Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys Phe Thr
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            260                 265                 270

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    290                 295                 300

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305                 310                 315                 320

Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser Ser Phe
                325                 330                 335

Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn Gly Gly
            340                 345                 350

Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln Pro Asp
        355                 360                 365

Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu Thr Gly
    370                 375                 380

Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn Ala Asp
385                 390                 395                 400

Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr Lys Glu
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Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr Thr Ser
            420                 425                 430

Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val Arg Val
        435                 440                 445

Arg Ser Lys Gln Arg Asn Ser Gly Asn Tyr Gly Glu Phe Ser Glu Val
    450                 455                 460

Leu Tyr Val Thr Leu Pro Gln Met Ser Gln Phe Thr Cys Glu Glu Asp
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Phe Tyr Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly Gly
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acaacgctag tctccgcgcc catcgtctgc accagctggc ctttgacacc taccaggagt 180

ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac ccccagacct 240

ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300

ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360

agttcctcag gagtgtcttc gccaacagcc tggtgtacgg cgcctctgac agcaacgtct 420

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gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac acaaactcac 540

acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg aaggacatgg 600

acaaggtcga gacattcctg cgcatcgtgc agtgccgctc tgtggagggc agctgtggct 660

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tccgcgccca tcgtctgcac cagctggcct ttgacaccta ccaggagttt gaagaagcct 840

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cagagtctat tccgacaccc tccaacaggg aggaaacaca acagaaatcc aacctagagc 960

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<213> Artificial Sequence

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Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
130 135 140

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Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
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Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
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Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Pro Thr Ile
225                 230                 235                 240

Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu
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His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile
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Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu
        275                 280                 285

Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln
    290                 295                 300

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln
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Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser
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Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser
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Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val
                405                 410                 415

Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly Gly Gly Asp
            420                 425                 430

Ile Asp Lys Leu Val Lys Cys Gly Gly Ile Ser Leu Leu Val Gln Asn
        435                 440                 445

Thr Ser Trp Met Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala
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Leu Asp Phe Ile Ser Leu
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<210> 9
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<212> DNA
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<220>
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SEQUENCE LISTING

<110> Ross, Richard
Sayers, Jon
Artymiuk, Peter

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<170> PatentIn version 3.5

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20 25 30

Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
130 135 140

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Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly
    210                 215                 220

Gly Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu
225                 230                 235                 240

Leu Ser Leu Ser Leu Leu Gln Ala Leu Asp Phe Ile Ser Leu
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aacttcaata caaagaagta aatgaaacta aatggaaaat gatggaccct atattgacaa 1320

catcagttcc agtgtactca ttgaaagtgg ataaggaata tgaagtgcgt gtgagatcca 1380

aacaacgaaa ctctggaaat tatggcgagt tcagtgaggt gctctatgta acacttcctc 1440

agatgagcca atttacatgt gaagaagatt tctacggcgg tggaggggat atcgacaagc 1500

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<210> 4
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein comprising growth hormone fused to growth hormone receptor

<400> 4

Met Asp Leu Trp Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser
1 5 10 15

Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
20 25 30

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Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
        35                  40                  45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
    50                  55                  60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65                  70                  75                  80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
                85                  90                  95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
            100                 105                 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
        115                 120                 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
    130                 135                 140

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Ser Gly Ser
225                 230                 235                 240

Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu Gln Ser
                245                 250                 255

Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys Phe Thr
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            260                 265                 270

Lys Cys Arg Ser Pro Glu Arg Glu Thr Phe Ser Cys His Trp Thr Asp
        275                 280                 285

Glu Val His His Gly Thr Lys Asn Leu Gly Pro Ile Gln Leu Phe Tyr
    290                 295                 300

Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu Cys Pro
305                 310                 315                 320

Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser Ser Phe
                325                 330                 335

Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn Gly Gly
            340                 345                 350

Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln Pro Asp
        355                 360                 365

Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu Thr Gly
    370                 375                 380

Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn Ala Asp
385                 390                 395                 400

Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr Lys Glu
                405                 410                 415

Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr Thr Ser
            420                 425                 430

Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val Arg Val
        435                 440                 445

Arg Ser Lys Gln Arg Asn Ser Gly Asn Tyr Gly Glu Phe Ser Glu Val
    450                 455                 460

Leu Tyr Val Thr Leu Pro Gln Met Ser Gln Phe Thr Cys Glu Glu Asp
465                 470                 475                 480

Phe Tyr Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly Gly
                485                 490                 495
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Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu Leu
500 505 510

Ser Leu Ser Leu Leu Gln Ala Leu Asp Phe Ile Ser Leu
515 520 525

<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
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cactggcagg atcaagtgat gctcatatgt tcccaaccat tcccttatcc aggctttttg 120

acaacgctag tctccgcgcc catcgtctgc accagctggc ctttgacacc taccaggagt 180

ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac ccccagacct 240

ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300

ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360

agttcctcag gagtgtcttc gccaacagcc tggtgtacgg cgcctctgac agcaacgtct 420

atgacctcct aaaggaccta gaggaaggca tccaaacgct gatggggagg ctggaagatg 480

gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac acaaactcac 540

acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg aaggacatgg 600

acaaggtcga gacattcctg cgcatcgtgc agtgccgctc tgtggagggc agctgtggct 660

tcggcggccg cggtggcgga ggtagtggtg gcggaggtag cggtggcgga ggttctggtg 720

gcggaggttc cgaattcttc ccaaccattc ccttatccag gctttttgac aacgctagtc 780

tccgcgccca tcgtctgcac cagctggcct ttgacaccta ccaggagttt gaagaagcct 840

atatcccaaa ggaacagaag tattcattcc tgcagaaccc ccagacctcc ctctgtttct 900

cagagtctat tccgacaccc tccaacaggg aggaaacaca acagaaatcc aacctagagc 960

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cattcctgcg catcgtgcag tgccgctctg tggagggcag ctgtggcttc ggcggtggag 1320

gggatatcga caagctggtc aagtgtggcg gcataagcct gctggttcag aacacatcct 1380

ggatgctgct gctgctgctt tccctctccc tcctccaagc cctagacttc atttctctgt 1440

ga 1442

<210> 6
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein comprising growth hormone fused to growth hormone

<400> 6

Met Asp Leu Trp Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser
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Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
20 25 30

Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
130 135 140

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Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Pro Thr Ile
225                 230                 235                 240

Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu
                245                 250                 255

His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile
            260                 265                 270

Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu
        275                 280                 285

Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln
    290                 295                 300

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln
305                 310                 315                 320

Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser
                325                 330                 335

Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp
            340                 345                 350

Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser
        355                 360                 365
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Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr
    370                 375                 380

Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr
385                 390                 395                 400

Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val
                405                 410                 415

Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly Gly Gly Asp
            420                 425                 430

Ile Asp Lys Leu Val Lys Cys Gly Gly Ile Ser Leu Leu Val Gln Asn
        435                 440                 445

Thr Ser Trp Met Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala
    450                 455                 460

Leu Asp Phe Ile Ser Leu
465                 470
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<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> growth hormone receptor primer

<400> 7
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<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> growth hormone receptor primer

<400> 8
gcgccatatg agcatcactt gatcctgcg 29

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer amplification of human growth hormone

<400> 9
gcgccatatg ttcccaacca ttcccttatc

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<110> Ross, Richard
Sayers, Jon
Artymiuk, Peter

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acaacgctag tctccgcgcc catcgtctgc accagctggc ctttgacacc taccaggagt 180

ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac ccccagacct 240

ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300

ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360

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gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac acaaactcac 540

acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg aaggacatgg 600

acaaggtcga gacattcctg cgcatcgtgc agtgccgctc tgtggagggc agctgtggct 660

tcggcggtgg aggggatatc gacaagctgg tcaagtgtgg cggcataagc ctgctggttc 720

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<210> 2
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein comprising growth hormone fused to a glycosylphosphatidyinositol domain

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Met Asp Leu Trp Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser
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Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
20 25 30

Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
130 135 140

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Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly
    210                 215                 220

Gly Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu
225                 230                 235                 240

Leu Ser Leu Ser Leu Leu Gln Ala Leu Asp Phe Ile Ser Leu
                245                 250
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<211> 1607
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein comprising growth hormone fused to growth hormone receptor

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acaacgctag tctccgcgcc catcgtctgc accagctggc ctttgacacc taccaggagt 180

ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac ccccagacct 240

ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300

ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360

agttcctcag gagtgtcttc gccaacagcc tggtgtacgg cgcctctgac agcaacgtct 420

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gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac acaaactcac 540

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tcggcggccg cggtggcgga ggtagtggtg gcggaggtag cggtggcgga ggttctggtg 720

gcggaggttc cgaattcttt tctggaagtg aggccacagc agctatcctt agcagagcac 780

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catcagttcc agtgtactca ttgaaagtgg ataaggaata tgaagtgcgt gtgagatcca 1380

aacaacgaaa ctctggaaat tatggcgagt tcagtgaggt gctctatgta acacttcctc 1440

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tgctttccct ctccctcctc caagccctag acttcatttc tctgtga 1607

<210> 4
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein comprising growth hormone fused to growth hormone receptor

<400> 4

Met Asp Leu Trp Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser
1 5 10 15

Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
20 25 30

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Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
        35                  40                  45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
    50                  55                  60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65                  70                  75                  80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
                85                  90                  95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
            100                 105                 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
        115                 120                 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
    130                 135                 140

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Ser Gly Ser
225                 230                 235                 240

Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu Gln Ser
                245                 250                 255

Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys Phe Thr
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            260                 265                 270

Lys Cys Arg Ser Pro Glu Arg Glu Thr Phe Ser Cys His Trp Thr Asp
        275                 280                 285

Glu Val His His Gly Thr Lys Asn Leu Gly Pro Ile Gln Leu Phe Tyr
    290                 295                 300

Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu Cys Pro
305                 310                 315                 320

Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser Ser Phe
                325                 330                 335

Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn Gly Gly
            340                 345                 350

Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln Pro Asp
        355                 360                 365

Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu Thr Gly
    370                 375                 380

Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn Ala Asp
385                 390                 395                 400

Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr Lys Glu
                405                 410                 415

Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr Thr Ser
            420                 425                 430

Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val Arg Val
        435                 440                 445

Arg Ser Lys Gln Arg Asn Ser Gly Asn Tyr Gly Glu Phe Ser Glu Val
    450                 455                 460

Leu Tyr Val Thr Leu Pro Gln Met Ser Gln Phe Thr Cys Glu Glu Asp
465                 470                 475                 480

Phe Tyr Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly Gly
                485                 490                 495
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Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu Leu
500 505 510

Ser Leu Ser Leu Leu Gln Ala Leu Asp Phe Ile Ser Leu
515 520 525

<210> 5
<211> 1442
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein comprising growth hormone fused to growth hormone

<400> 5
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acaacgctag tctccgcgcc catcgtctgc accagctggc ctttgacacc taccaggagt 180

ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac ccccagacct 240

ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300

ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360

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acaaggtcga gacattcctg cgcatcgtgc agtgccgctc tgtggagggc agctgtggct 660

tcggcggccg cggtggcgga ggtagtggtg gcggaggtag cggtggcgga ggttctggtg 720

gcggaggttc cgaattcttc ccaaccattc ccttatccag gctttttgac aacgctagtc 780

tccgcgccca tcgtctgcac cagctggcct ttgacaccta ccaggagttt gaagaagcct 840

atatcccaaa ggaacagaag tattcattcc tgcagaaccc ccagacctcc ctctgtttct 900

cagagtctat tccgacaccc tccaacaggg aggaaacaca acagaaatcc aacctagagc 960

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ga 1442

<210> 6
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
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<400> 6

Met Asp Leu Trp Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser
1 5 10 15

Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
20 25 30

Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
130 135 140

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Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Pro Thr Ile
225                 230                 235                 240

Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu
                245                 250                 255

His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile
            260                 265                 270

Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu
        275                 280                 285

Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln
    290                 295                 300

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln
305                 310                 315                 320

Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser
                325                 330                 335

Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp
            340                 345                 350

Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser
        355                 360                 365
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Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr
    370                 375                 380

Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr
385                 390                 395                 400

Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val
                405                 410                 415

Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly Gly Gly Asp
            420                 425                 430

Ile Asp Lys Leu Val Lys Cys Gly Gly Ile Ser Leu Leu Val Gln Asn
        435                 440                 445

Thr Ser Trp Met Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala
    450                 455                 460

Leu Asp Phe Ile Ser Leu
465                 470
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<212> DNA
<213> Artificial Sequence

<220>
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<213> Artificial Sequence

<220>
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gcgccatatg agcatcactt gatcctgcg 29

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer amplification of human growth hormone

<400> 9
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SEQUENCE LISTING

<110> Ross, Richard
Sayers, Jon
Artymiuk, Peter

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<150> 10/552,388
<151> 2005-10-07

<150> PCT/GB04/001572
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<150> GB 0324235.1
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acaacgctag tctccgcgcc catcgtctgc accagctggc ctttgacacc taccaggagt 180

ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac ccccagacct 240

ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300

ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360

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gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac acaaactcac 540

acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg aaggacatgg 600

acaaggtcga gacattcctg cgcatcgtgc agtgccgctc tgtggagggc agctgtggct 660

tcggcggtgg aggggatatc gacaagctgg tcaagtgtgg cggcataagc ctgctggttc 720

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<210> 2
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
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Met Asp Leu Trp Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser
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Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
20 25 30

Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
130 135 140

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Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly
    210                 215                 220

Gly Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu
225                 230                 235                 240

Leu Ser Leu Ser Leu Leu Gln Ala Leu Asp Phe Ile Ser Leu
                245                 250
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<210> 3
<211> 1607
<212> DNA
<213> Artificial Sequence

<220>
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<400> 3
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acaacgctag tctccgcgcc catcgtctgc accagctggc ctttgacacc taccaggagt 180

ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac ccccagacct 240

ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300

ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360

agttcctcag gagtgtcttc gccaacagcc tggtgtacgg cgcctctgac agcaacgtct 420

atgacctcct aaaggaccta gaggaaggca tccaaacgct gatggggagg ctggaagatg 480

gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac acaaactcac 540

acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg aaggacatgg 600

acaaggtcga gacattcctg cgcatcgtgc agtgccgctc tgtggagggc agctgtggct 660

tcggcggccg cggtggcgga ggtagtggtg gcggaggtag cggtggcgga ggttctggtg 720

gcggaggttc cgaattcttt tctggaagtg aggccacagc agctatcctt agcagagcac 780

cctggagtct gcaaagtgtt aatccaggcc taaagacaaa ttcttctaag gagcctaaat 840

tcaccaagtg ccgttcacct gagcgagaga ctttttcatg ccactggaca gatgaggttc 900

atcatggtac aaagaaccta ggacccatac agctgttcta taccagaagg aacactcaag 960

aatggactca agaatggaaa gaatgccctg attatgtttc tgctggggaa aacagctgtt 1020

actttaattc atcgtttacc tccatctgga taccttattg tatcaagcta actagcaatg 1080

gtggtacagt ggatgaaaag tgtttctctg ttgatgaaat agtgcaacca gatccaccca 1140

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aacaacgaaa ctctggaaat tatggcgagt tcagtgaggt gctctatgta acacttcctc 1440

agatgagcca atttacatgt gaagaagatt tctacggcgg tggaggggat atcgacaagc 1500

tggtcaagtg tggcggcata agcctgctgg ttcagaacac atcctggatg ctgctgctgc 1560

tgctttccct ctccctcctc caagccctag acttcatttc tctgtga 1607

<210> 4
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
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<400> 4

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1 5 10 15

Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
20 25 30

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Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
        35                  40                  45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
    50                  55                  60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65                  70                  75                  80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
                85                  90                  95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
            100                 105                 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
        115                 120                 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
    130                 135                 140

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Ser Gly Ser
225                 230                 235                 240

Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu Gln Ser
                245                 250                 255

Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys Phe Thr
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            260                 265                 270

Lys Cys Arg Ser Pro Glu Arg Glu Thr Phe Ser Cys His Trp Thr Asp
        275                 280                 285

Glu Val His His Gly Thr Lys Asn Leu Gly Pro Ile Gln Leu Phe Tyr
    290                 295                 300

Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu Cys Pro
305                 310                 315                 320

Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser Ser Phe
                325                 330                 335

Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn Gly Gly
            340                 345                 350

Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln Pro Asp
        355                 360                 365

Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu Thr Gly
    370                 375                 380

Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn Ala Asp
385                 390                 395                 400

Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr Lys Glu
                405                 410                 415

Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr Thr Ser
            420                 425                 430

Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val Arg Val
        435                 440                 445

Arg Ser Lys Gln Arg Asn Ser Gly Asn Tyr Gly Glu Phe Ser Glu Val
    450                 455                 460

Leu Tyr Val Thr Leu Pro Gln Met Ser Gln Phe Thr Cys Glu Glu Asp
465                 470                 475                 480

Phe Tyr Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly Gly
                485                 490                 495
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Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu Leu
500 505 510

Ser Leu Ser Leu Leu Gln Ala Leu Asp Phe Ile Ser Leu
515 520 525

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<211> 1442
<212> DNA
<213> Artificial Sequence

<220>
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<400> 5
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acaacgctag tctccgcgcc catcgtctgc accagctggc ctttgacacc taccaggagt 180

ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac ccccagacct 240

ccctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300

ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360

agttcctcag gagtgtcttc gccaacagcc tggtgtacgg cgcctctgac agcaacgtct 420

atgacctcct aaaggaccta gaggaaggca tccaaacgct gatggggagg ctggaagatg 480

gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac acaaactcac 540

acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg aaggacatgg 600

acaaggtcga gacattcctg cgcatcgtgc agtgccgctc tgtggagggc agctgtggct 660

tcggcggccg cggtggcgga ggtagtggtg gcggaggtag cggtggcgga ggttctggtg 720

gcggaggttc cgaattcttc ccaaccattc ccttatccag gctttttgac aacgctagtc 780

tccgcgccca tcgtctgcac cagctggcct ttgacaccta ccaggagttt gaagaagcct 840

atatcccaaa ggaacagaag tattcattcc tgcagaaccc ccagacctcc ctctgtttct 900

cagagtctat tccgacaccc tccaacaggg aggaaacaca acagaaatcc aacctagagc 960

tgctccgcat ctccctgctg ctcatccagt cgtggctgga gcccgtgcag ttcctcagga 1020

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aggacctaga ggaaggcatc caaacgctga tggggaggct ggaagatggc agcccccgga 1140

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cactactcaa gaactacggg ctgctctact gcttcaggaa ggacatggac aaggtcgaga 1260

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gggatatcga caagctggtc aagtgtggcg gcataagcct gctggttcag aacacatcct 1380

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ga 1442

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<212> PRT
<213> Artificial Sequence

<220>
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<400> 6

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Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
20 25 30

Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
130 135 140

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Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
145                 150                 155                 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
                165                 170                 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
            180                 185                 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
        195                 200                 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Pro Thr Ile
225                 230                 235                 240

Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu
                245                 250                 255

His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile
            260                 265                 270

Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu
        275                 280                 285

Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln
    290                 295                 300

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln
305                 310                 315                 320

Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser
                325                 330                 335

Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp
            340                 345                 350

Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser
        355                 360                 365
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Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr
    370                 375                 380

Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr
385                 390                 395                 400

Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val
                405                 410                 415

Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly Gly Gly Asp
            420                 425                 430

Ile Asp Lys Leu Val Lys Cys Gly Gly Ile Ser Leu Leu Val Gln Asn
        435                 440                 445

Thr Ser Trp Met Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala
    450                 455                 460

Leu Asp Phe Ile Ser Leu
465                 470
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<210> 7
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<223> growth hormone receptor primer

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<210> 8
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gcgccatatg agcatcactt gatcctgcg 29

<210> 9
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<212> DNA
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<223> primer amplification of human growth hormone

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gcgccatatg ttcccaacca ttcccttatc